APPLICANT(S): Lyapina et al.
TITLE: REGULATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER PROTEINS
Application No.: 10/046,961 File Date: January 14, 2002
Docket No.: CIT1510-3


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AMSH1   THNEFTITHVIVP--KQSAGPDYCDMENVEELFNVQDQHD--LLTLGWIHTHPTQTAFLS
AMSH2   THNEFTITHVIVP--KQSAGPDYCDMENVEELFNVQDQHD--LLTLGWIHTHPTQTAFLS
AMSH    MRNEFTITHVLIP--KQSAGSDYCNTENEEELFLIQDQQG--LITLGWIHTHPTQTAFLS
Rpn11   TVRVIDVFAMPQS--GTGVSVEAVDPVFQAKMLDMLKQTGRPEMVVGWYHSHPGFGCWLS
Jab1    TMIIMDSFALPVEGTETRVNAQAAAYEYMAAYIENAKQVGRLENAIGWYHSHPGYGCWLS
            :    :         .. :          :   .* .    .:** *:*    .:**

AMSH1   SVDLHTHCSYQLMLPEAIAIVCSPKHKDTG-----IFRLTNAGMLEVSACKKKGFH--PH
AMSH2   SVDLHTHCSYQLMLPEAIAIVCSPKHKDTG-----IFRLTNAGMLEVSACKKKGFH--PH
AMSH    SVDLHTHCSYQMMLPESVAIVCSPKFQETG-----FFKLTDHGLEEISSCRQKGFH--PH
Rpn11   GVDINTQQSFEALSERAVAVVVDPIQSVKGKVVIDAFRLINANMMVLGHEPRQTTSNLGH
Jab1    GIDVSTQMLNQQFQEPFVAVVIDPTRTISAG----KVNLGAFRTYPKGYKPPDEGPSEYQ
        .:*: *:   : :    :*:* .*    ..       ..*         .    .      :

AMSH1   TKEPRLFSICKHV--LVKDIKI----------IVLDLR----------------------
AMSH2   TKEPRLFSIQKFLSGIISGTAL----------EMEPLKIGYGPNGFPLLGISRSSSPSEQ
AMSH    SKDPPLFCSCSHVT--VVDRAV----------TITDLR----------------------
Rpn11   LNKPSIQALIHGLNRHYYSITINYRKNELEQKMLLNLHKKSWMEGLTLQDYSEHCKHNES
Jab1    TIPLNKIEDFGVHCKQYYALEVSYFKSSLDRKLLELLWNKYWVNTLSSSSLLTNADYTTG
                           :           :  *

AMSH1   ------------------------------------------------------------
AMSH2   L-----------------------------------------------------------
AMSH    ------------------------------------------------------------
Rpn11   VVKEMLELAKNYNKAVEEEDKMTPEQLAIKNVGKQDPKRHLEEHVDVLMTSNIVQCLAAM
Jab1    QVFDLSEKLEQSEAQLGRGSFMLG--LETHDRKSEDKLAKATRDSCKTTIEAIHGLMSQV

AMSH1   ------------
AMSH2   ------------
AMSH    ------------
Rpn11   LDTVVFK-----
Jab1    IKDKLFNQINIS
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FIG. 1

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AMSH1   ---------------MPDHTDVSLSPEERVRALSKLGCNITISEDITPRR 35
AMSH2   MDQPFTVNSLKKLAAMPDHTDVSLSPEERVRALSKLGCNITISEDITPRR 50
AMSH    ---------------MSDHGDVSLPPEDRVRALSQLGSAVEVNEDIPPRR 35
                       *.** ****.**:******:**. : :.***.***

AMSH1   YFRSGVEMERMASVYLEEGNLENAFVLYNKFITLFVEKLPNHRDYQQCAV 85
AMSH2   YFRSGVEMERMASVYLEEGNLENAFVLYNKFITLFVEKLPNHRDYQQCAV 100
AMSH    YFRSGVEIIRMASIYSEEGNIEHAFILYNKYITLFIEKLPKHRDYKSAVI 85
        *******: ****:* ****:*:**:****:****:****:****:...:

AMSH1   PEKQDIMKKLKEIAFPRTDELKNDLLKKYNVEYQEYLQSKNKYKAEILKK 135
AMSH2   PEKQDIMKKLKEIAFPRTDELKNDLLKKYNVEYQEYLQSKNKYKAEILKK 150
AMSH    PEKKDTVKKLKEIAFPKAEELKAELLKRYTKEYTEYNEEKKKEAEELARN 135
        ***:* :*********:::*** :***:*. ** ** :.*:*   *: ::

AMSH1   LEHQRLIEAERKRIAQMRQQQLESEQFLFFEDQLKKQELARGQMRSQQTS 185
AMSH2   LEHQRLIEAERKRIAQMRQQQLESEQFLFFEDQLKKQELARGQMRSQQTS 200
AMSH    MAIQQELEKEKQRVAQQKQQQLEQEQFHAFEEMIRNQELEKERLKIVQEF 185
        :  *: :* *::*:** :*****.***  **: :::*** : :::  *

AMSH1   G-LSEQIDGSALSCFS--THQNNSLLNVFADQPNKSDATNYASHSPPVNR 232
AMSH2   G-LSEQIDGSALSCFS--THQNNSLLNVFADQPNKSDATNYASHSPPVNR 247
AMSH    GKVDPGLGGPLVPDLEKPSLDVFPTLTVSSIQPSDCHTTVRPAKPPVVDR 235
        * :.  :.*. :. :.  : :  . *.* : **....:*  .::.* *:*

AMSH1   ALTPAATLSAVQNLVVEGLRCVVLPEDLCHKFLQLAESNTVRGIETCGIL 282
AMSH2   ALTPAATLSAVQNLVVEGLRCVVLPEDLCHKFLQLAESNTVRGIETCGIL 297
AMSH    SLKPGALSNSESIPTIDGLRHVVVPGRLCPQFLQLASANTARGVETCGIL 285
        :*.*.*  .: .  .::*** **:*  ** :*****.:**.**:******

AMSH1   CGKLTHNEFTITHVIVPKQSAGPDYCDMENVEELFNVQDQHDLLTLGWIH 332
AMSH2   CGKLTHNEFTITHVIVPKQSAGPDYCDMENVEELFNVQDQHDLLTLGWIH 347
AMSH    CGKLMRNEFTITHVLIPKQSAGSDYCNTENEEELFLIQDQQGLITLGWIH 335
        **** :********::******.***: ** **** :***:.*:*****

AMSH1   THPTQTAFLSSVDLHTHCSYQLMLPEAIAIVCSPKHKDTGIFRLTNAGML 382
AMSH2   THPTQTAFLSSVDLHTHCSYQLMLPEAIAIVCSPKHKDTGIFRLTNAGML 397
AMSH    THPTQTAFLSSVDLHTHCSYQMMLPESVAIVCSPKFQETGFFKLTDHGLE 385
        **********:********:****::*******.::**:*:**: *:

AMSH1   EVSACKKKGFHPHTKEPRLFSICKHV--LVKDIKIIVLDLR--------- 421
AMSH2   EVSACKKKGFHPHTKEPRLFSIQKFLSGIISGTALEMEPLKIGYGPNGFP 447
AMSH    EISSCRQKGFHPHSKDPPLFCSCSHVT--VVDRAVTITDLR--------- 424
        *:*:*::******:*:* **.  ..:   : .  : :  *:

AMSH1   --------------
AMSH2   LLGISRSSSPSEQL 461
AMSH    --------------
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FIG. 2

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COP9_su5_Hs     VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQQFQEPFVA--VVIDPTRTISAGKVNLG
COP9_su5_Dm     VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG
COP9_su5_At     AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQQHQEPFLA--VVIDPTRTVSAGKVEIG
cop9_su5_Ce     EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG
AF2198_Arcfu    LPIGMKVFGTVHSHPSPSCRPSEEDLSLFTRFGKYHIIVCY--PYDENSWKCYNRKGEEV
PH0451_Pyrho    MPHDESIKGTFHSHPSPFPYPSEGDLMFFSKFGGIHIIAAF--PYDEDSVKAFDSEGREV
TVN1035_Thevo   KPIDFSLVGSVHSHPSGITKPSDEDLRMFSLTGKIHIIVGY--PYNLKDYSAYDRSGNKV
MTH971_Metth    LPPFTGAVGSVHSHPGPVNLPSAADLHFFSKNGLFHLIIAH--PYTMETVAAYTRNGDPV
aq_1691_Aquae   ISKGMEIVGVYHSHPDHPDRPSQFDLQRAFPDLSYIIFSVQ--KGKVASYRSWELKGDKF
RV1334_Myctu    EDADEVPVVIYHSHTATEAYPSRTDVKLATEPDAHYVLVSTRDPHRHELRSYRIVDGAVT
RadC_Ecoli      IKINASALILAHNHPSGCAEPSKADKLITERIIKSCQFMDL--RVLDHIVIGRGEYVSFA
  ''''''''''''''''''''''''''''HSHP''''''S ''D
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FIG. 3

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COP9_su5_Hs     VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQQFQEPFVA--VVIDPTRTISAGKVNLG
COP9_su5_Dm     VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG
COP9_su5_At     AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQQHQEPFLA--VVIDPTRTVSAGKVEIG
cop9_su5_Ce     EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG
Pad1_Dm         TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
Pad1_Hs         TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
Sks1_Dd         TGRDEIVIGWYHSHPGFGCWLSSVDVNTQQSFEQLQSRAVA--VVVDPLQSVRG-KVVID
Pad1_Sc         TGRDQMVVGWYHSHPGFGCWLSSVDVNTQKSFEQLNSRAVA--VVVDPIQSVKG-KVVID
''''''''''''''''''''''''''''' HSHP''''''S 'D
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FIG. 4